



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 147441

TO: Amy H Bowman
Location: REM/2C18
Art Unit: 1635
Tuesday, March 22, 2005

Case Serial Number: 10/646391

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Bowman,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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STIC-Biotech/ChemLib

147441

From: Bowman, Amy
Sent: Thursday, March 10, 2005 3:29 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/646,391 (2)

Hello,
I need SEQ ID NO:4 searched from application number 10/646,391.
Thank you,
Amy Bowman
AU 1635

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MAR 10 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 07:42:25 ; Search time 1430 Seconds
(without alignments)
711.580 Million cell updates/sec

Title: US-10-646-391A-4
Perfect score: 21
Sequence: 1 cagcagcagagtcttcacat 21
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	6	CQ786615 Sequence
2	21	100.0	23	6	CQ786178 Sequence
3	21	100.0	181	6	AR302789 Sequence
4	21	100.0	195	6	AR302784 Sequence
5	21	100.0	255	6	CQ693037 Sequence
6	21	100.0	270	6	CQ688092 Sequence
7	21	100.0	275	6	AX895152 Sequence
8	21	100.0	275	6	BD030685 Sequence
9	21	100.0	306	6	CQ684015 Sequence
10	21	100.0	396	6	AR391192 Sequence
11	21	100.0	396	6	AR392897 Sequence
12	21	100.0	396	6	AR489627 Sequence
13	21	100.0	396	6	AX493868 Sequence
14	21	100.0	396	6	AX093197 Sequence
15	21	100.0	482	6	AR421770 Sequence
16	21	100.0	482	6	AX982464 Sequence
17	21	100.0	482	6	BD117323 EST and e
18	21	100.0	491	6	AX887886 Sequence
19	21	100.0	491	6	BD027496 Sequence

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C 22	21	100.0	1589	6	AX600212	Sequence
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C 34	21	100.0	1684	9	BC010514	Homo sapi
C 35	21	100.0	1712	6	AX600209	Sequence
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C 43	21	100.0	175380	9	AF235104	Homo sapi
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ALIGNMENTS

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LOCUS	Sequence 4 from Patent WO2004018675.				
DEFINITION	CQ786615				
ACCESSION	CQ786615.1	GI:45721635			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Jansen, B.				
TITLE	Treatment of melanoma by reduction in clusterin levels				
JOURNAL	Patent: WO 2004018675-A 4 04-MAR-2004;				
FEATURES	The University of British Columbia (CA); Gleave, Martin E. (CA)				
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LOCUS	Sequence 66 from Patent WO2004018676.				
DEFINITION	CQ786178				
ACCESSION	CQ786178.1	GI:45721281			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

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ACCESSION     CQ693037
VERSION       CQ693037.1 GI:42234544
KEYWORDS
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1 Liew,C.C., Marshall,W.E. and Zhang,H.
AUTHORS      Compositions and methods relating to osteoarthritis
TITLE        Patent: WO 02070737-A 37963 12-SEP-2002;
JOURNAL      Chondrogene Inc. (CA)

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QY      1 CAGCAGCAGAGTCTTCATCAT 21
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LOCUS           Homo sapiens (human)                linear      PAT 03-FEB-2004
DEFINITION     Sequence 33018 from Patent WO02070737.    270 bp   DNA
ACCESSION     CQ688092
VERSION       CQ688092.1 GI:42219840
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1 Liew,C.C., Marshall,W.E. and Zhang,H.
AUTHORS      Compositions and methods relating to osteoarthritis
TITLE        Patent: WO 02070737-A 33018 12-SEP-2002;
JOURNAL      Chondrogene Inc. (CA)

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LOCUS
DEFINITION Sequence 11015 from Patent EP1033401.
ACCESSION AX895152
VERSION AX895152.1 GI:40050036
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 11015 06-SEP-2000;
Genset (FR)
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ACCESSION BD030685
VERSION BD030685.1 GI:22572427
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 6931 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/6931
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68 /G06F17/30, C12N15/00, C12N5/00, PC
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ACCESSION AX895152
VERSION AX895152.1 GI:40050036
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 11015 06-SEP-2000;
Genset (FR)
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LOCUS
DEFINITION Sequence 15 from patent US 6613515.
ACCESSION AR391192
VERSION AR391192.1 GI:40114652
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE Xu, J. and Stolk, J.A.
AUTHORS Ovarian tumor sequences and methods of use therefor
TITLE Patent: US 6613515-A 15 02-SEP-2003;
JOURNAL
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VERSION AR392897.1 GI:40118137
KEYWORDS

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VERSION CQ684015.1 GI:42207944
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 28941 12-SEP-2002;
Chondrogene Inc. (CA)
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LOCUS
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ACCESSION AR391192
VERSION AR391192.1 GI:40114652
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE Xu, J. and Stolk, J.A.
AUTHORS Ovarian tumor sequences and methods of use therefor
TITLE Patent: US 6613515-A 15 02-SEP-2003;
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RESULT 11
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LOCUS
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ACCESSION AR392897
VERSION AR392897.1 GI:40118137
KEYWORDS

Search completed: March 22, 2005, 10:29:00
Job time : 1433 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 04:56:41 ; Search time 235 Seconds
(without alignments)
528.998 Million cell updates/sec

Title: US-10-646-391A-4

Perfect score: 21

Sequence: 1 cagcagcagatgtcttcatcat 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: Geneseqn2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	21	100.0	21	11	ADM83069 Human TRP
4	21	100.0	21	12	ADL70406 Antisense
5	21	100.0	23	12	ADL70521 Human clu
6	21	100.0	195	2	ANT00416 Genetic B
7	21	100.0	275	3	AAC06940 Human sec
8	21	100.0	396	4	AAF94824 Human ova
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ALIGNMENTS

RESULT 1

AAA94226

ID AAA94226 standard; DNA; 21 BP.

XX AAA94226;

DT 12-JAN-2001 (first entry)

XX Human testosterone-repressed prostate message-2 antisense oligo #2.

XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
OS Homo sapiens.
XX WO200049937-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US004875.
XX 26-FEB-1999; 99US-0121726P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX Claim 3; Page 36; 38pp; English.
XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective

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Best Local Similarity 100.0%; Pred. No. 8.2;
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ID ACF36398 standard; DNA; 21 BP.
XX AC ACF36398;
XX DT 18-DEC-2003 (first entry)
XX DE TRPM-2 antisense oligonucleotide.
XX KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
XX KW prostate cancer; anti-apoptotic protein; antisense; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003072591-A1.
XX PD 04-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US005305.
XX PR 22-FEB-2002; 2002US-00080794.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX WPI; 2003-689981/65.
XX DR New modified antisense oligonucleotide, useful particularly for treating
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX PS Claim 1; Page 25; 44pp; English.
XX CC The invention relates to a compound consisting of an oligonucleotide with
CC a phosphorothioate backbone throughout, in which: (a) sugars on
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC prostatic cancer cells to the androgen-independent state, in vivo or in
CC vitro; (b) to treat prostatic cancer (after initially withdrawing
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC ovarian and some breast cancer cells) that express abnormal levels of
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC increase stability in vivo and activity (both in vivo or in vitro) and
CC result in a synergistic increase in effect when (I) is used with
CC chemotherapeutic agents or other antisense oligonucleotides directed
CC against other antiapoptotic genes. The present sequence represents a
CC specific example of an anti-apoptotic protein TRPM-2 (testosterone-
CC repressed prostate message-2) antisense oligonucleotide
XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
```

```
Db 1 CAGCAGCAGAGTCTTCATCAT 21
RESULT 3
ADM83069
ID ADM83069 standard; DNA; 21 BP.
XX AC ADM83069;
XX DT 03-JUN-2004 (first entry)
XX DE Human TRPM-2 antisense oligonucleotide #4.
XX KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
XX KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
XX KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
XX KW antisense; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX PN US2003158130-A1.
XX PD 21-AUG-2003.
XX PF 28-SEP-2001; 2001US-00967726.
XX PR 25-FEB-2000; 2000WO-US004875.
XX PR 28-SEP-2000; 2000US-0236301P.
XX PR 10-AUG-2001; 2001US-00913325.
XX PA (GLEA/) GLEAVE M.
XX PA (RENN/) RENNIE P S.
XX PA (MIYA/) MIYAKE H.
XX PA (NELS/) NELSON C.
XX PA (ZELL/) ZELLWEGER T.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX WPI; 2003-778017/73.
XX DR Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT comprises administering a composition that inhibits expression of TRPM-2.
XX PS Claim 4; SEQ ID NO 4; 14pp; English.
XX CC The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is human testosterone-repressed prostate message-2 (TRPM
CC -2) antisense oligodeoxyribonucleotide (ODN).
XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 1 CAGCAGCAGAGTCTTCATCAT 21
```

CC sensitivity to subsequent treatment with cisplatin. A claimed method for
 CC regulating expression of bcl-xL in a subject or cell line comprises
 CC administering an agent effective to modulate the amount of clusterin
 CC expression. In clusterin-expressing cells, expression of bcl-xL is down-
 CC regulated when the effective amount of clusterin is reduced. Such
 CC inhibition is significant because bcl-xL is known to act as an inhibitor
 CC of apoptosis.
 CC
 XX
 SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCAGCAGAGTCTTCATCAT 21
 Db 1 CAGCAGCAGAGTCTTCATCAT 21
 RESULT 5
 ADL70521/c
 ID ADL70521 standard; cDNA; 23 BP.
 XX
 AC ADL70521;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human clusterin target for RNAi.
 XX
 KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
 KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;
 KW ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO2004018676-A2.
 XX
 PD 04-MAR-2004.
 XX
 PF 21-AUG-2003; 2003WO-CA001277.
 XX
 PR 21-AUG-2002; 2002US-0405193P.
 PR 03-SEP-2002; 2002US-0408152P.
 PR 20-MAY-2003; 2003US-0472387P.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trogakos IP;
 PI Gonos ES;
 XX
 WPI; 2004-226852/21.
 XX
 PT New RNA molecule less than 49 bases and having a sequence effective to
 PT mediate degradation or block translation of mRNA that is the
 PT transcriptional product of a target gene, useful for treating Alzheimer's
 PT disease or cancer.
 XX
 PS Example 6; SEQ ID NO 66; 63pp; English.
 XX
 CC The present sequence is a human clusterin cDNA target for a double-
 CC stranded short interfering RNA (siRNA) of the invention ADL70522-
 CC ADL70523. It was used in an example from the invention to demonstrate
 CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
 CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
 CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
 CC tumour cells following androgen withdrawal, and has also been shown to be
 CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
 CC siRNAs of the invention can be used alone or in combination with other
 CC chemotherapies or apoptosis inducing treatments for the treatment of
 CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
 CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
 CC anaplastic large cell lymphoma and melanoma, and also for the treatment

RESULT 4
 ADL70406
 ID ADL70406 standard; DNA; 21 BP.
 XX
 AC ADL70406;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Antisense oligonucleotide to human clusterin.
 XX
 KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..21
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate nucleotides"
 FT modified_base 1..4
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-methoxyethyl modifications"
 FT modified_base 18..21
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-O-methoxyethyl modifications"
 XX
 PN WO2004018675-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 21-AUG-2003; 2003WO-CA001276.
 XX
 PR 21-AUG-2002; 2002US-0405193P.
 PR 03-SEP-2002; 2002US-0408152P.
 PR 02-DEC-2002; 2002US-0319748P.
 PR 20-MAY-2003; 2003US-0472387P.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (GLEA/) GLEAVE M E.
 XX
 PI Jansen B;
 XX
 WPI; 2004-226851/21.
 XX
 PT Treating melanoma in a mammalian subject comprises administering to the
 PT subject a therapeutic agent effective to reduce the effective amount of
 PT clusterin in the melanoma cells.
 XX
 PS Claim 7; SEQ ID NO 4; 32pp; English.
 XX
 CC The present sequence is that of an antisense oligonucleotide targeted to
 CC human clusterin ADL70403. The invention relates to the treatment of
 CC melanoma through reduction in the effective amount of clusterin. The
 CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
 CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
 CC The antisense oligonucleotides are complementary to a region of the
 CC clusterin mRNA spanning either the translation initiation site or the
 CC termination site. They may be modified to increase stability in vivo,
 CC e.g. they may be employed as phosphorothioate derivatives and may have 2'
 CC -O- (2-methoxyethyl) (MOE) modifications in the 5' and 3' 'wings'. The
 CC present antisense oligonucleotide is particularly preferred. It is
 CC targeted to the translation initiation codon and next 6 codons of the
 CC human clusterin sequence. It has a phosphorothioate backbone throughout
 CC and MOE wings, the remaining nucleotides being 2'-deoxynucleotides. In an
 CC example from the invention, this antisense oligonucleotide provided a
 CC dose-dependent down-regulation of clusterin in human melanoma cells,
 CC leading to an increase in apoptotic cell death. In one melanoma cell line
 CC (607B) this alone was sufficient to lead to complete cell death. In
 CC another melanoma cell line, the surviving cells showed increased

CC of Alzheimer's disease.
 XX Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 21; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 DB 23 CAGCAGCAGAGTCTTCATCAT 3

RESULT 6
 AAT00416/c
 ID AAT00416 standard; cDNA; 195 BP.
 XX AC
 AC AAT00416;
 XX DT 26-MAR-1996 (first entry)
 XX Genetic suppressor element HL7.1.
 DE Genetic suppressor element; GSE; platinum-based drug; cisplatin;
 KW Chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2;
 KW BS.
 XX Synthetic.
 OS WO9522612-A2.
 XX PN 24-AUG-1995.
 XX PD 22-FEB-1995; 95WO-US0002303.
 XX PR 22-FEB-1994; 94US-00199900.
 XX PA (UNII) UNIV ILLINOIS FOUND.
 XX PI Kirschling DJ, Gudkov A, Roninson IB;
 XX WPI; 1995-302718/39.
 XX Genetic suppressor elements which confer resistance to platinum-based
 PT drugs, eg. cisplatin, on cancer cells - useful for enhancement of
 PT chemotherapy, and for diagnosis of resistance to these drugs.
 XX Claim 14; Fig 17; 75pp; English.

CC The sequences represented by AAT00405-T00418 are genetic suppressor
 CC elements (GSEs). This sequence represents GSE HL6.10. This sequence shows
 CC homology to the cDNA encoding testosterone-repressed prostatic message-2
 CC (TRPM-2). These sequences were obtained from a cDNA library derived from
 CC the total cDNA of a cisplatin sensitive cell. Genetic suppressor elements
 CC confer resistance to platinum-based drugs (pds), such as cisplatin. These
 CC functional GSEs can then be used to create probes for the parent gene.
 CC The probes can then be used in a method of measuring the level of GSE
 CC gene expression. The GSEs can be used in methods of diagnosis of
 CC resistance to pds by measuring the level of expression of GSE genes. The
 CC GSEs are also used in methods to overcome resistance to pds in cancer
 CC cells. The GSEs (or fragments of them) can be used to inhibit the
 CC function of genes associated with sensitivity to pds. For enhancement of
 CC chemotherapy, a GSE can be transferred (either alone or with another
 CC gene) on an expression vector into blood progenitor cells from a cancer
 CC patient. The cells are returned to the patients circulation and allowed
 CC to repopulate the blood before aggressive chemotherapy is carried out
 CC (using higher cisplatin concentrations than normal), this will thereby
 CC avoid toxic side effects to the immune system as the blood cells will be
 CC GSE resistant
 XX SQ Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 DB 128 CAGCAGCAGAGTCTTCATCAT 108

RESULT 7
 AAC06940/c
 ID AAC06940 standard; cDNA; 275 BP.
 XX AC
 AC AAC06940;
 XX DT 06-OCT-2000 (first entry)
 XX Human secreted protein 5' EST, SEQ ID NO: 11015.
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 KW Homo sapiens.
 OS EP1033401-A2.
 XX PN 06-SEP-2000.
 XX PD 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.
 XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX Claim 1; SEQ ID NO 11015; 71pp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors
 XX SQ Sequence 275 BP; 59 A; 88 C; 85 G; 43 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 275;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 DB 128 CAGCAGCAGAGTCTTCATCAT 108

RESULT 8
 AAF94824/c
 ID AAF94824 standard; cDNA; 396 BP.
 XX

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AC AAF94824;
XX DT 23-MAY-2001 (first entry)
XX DE Human ovarian cancer associated coding sequence SEQ ID NO: 15.
XX KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
XX OS Homo sapiens.
XX PN WO200118046-A2.
XX PD 15-MAR-2001.
XX PF 08-SEP-2000; 2000WO-US024827.
XX PR 10-SEP-1999; 99US-00394374.
XX PR 01-MAY-2000; 2000US-00561778.
XX PR 15-AUG-2000; 2000US-00640173.
XX PR 07-SEP-2000; 2000US-00656668.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Stolk JA;
XX DR WPI; 2001-211395/21.
XX PT Isolated polypeptides associated with ovarian carcinomas, and the nucleic
XX PT acids that encode them, useful for the prevention diagnosis and treatment
XX PT of ovarian cancers.
XX PS Claim 18; Page 120; 189pp; English.
XX CC The present invention provides a number of coding sequences and proteins,
XX CC the over-expression of which is associated with ovarian carcinoma/cancer.
XX CC These can be used in the diagnosis, treatment and prevention of ovarian
XX CC cancer, optionally by gene therapy or in the form of a vaccine. The
XX CC present sequence is an example of one of these sequences
XX SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 9
ABL48774/c
ID ABL48774 standard; cDNA; 396 BP.
XX AC ABL48774;
XX DT 18-JUN-2002 (first entry)
XX DE Ovarian carcinoma sequence isolate 23657.1.
XX KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX KW ss.
XX OS Homo sapiens.
XX PN US2002004491-A1.
XX PD 10-JAN-2002.
XX PF 03-APR-2001; 2001US-00825294.
XX PR 10-SEP-1999; 99US-00394374.
XX PR 01-MAY-2000; 2000US-00561778.

PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
XX PA (XULJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGA/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PI Xu J, Stolk JA, Algate PA, Fling SP;
XX DR WPI; 2002-171027/22.
XX PT Ovarian tumor polypeptide and polynucleotide useful in diagnosis,
XX PT prevention and/or treatment of cancer, especially ovarian cancer.
XX PS Example 1; Page 43; 131pp; English.
XX CC The invention relates to ovarian tumour polynucleotides and polypeptides
XX CC that may be utilised in cancer therapy, for example in a vaccine or gene
XX CC therapy. Polypeptides and polynucleotides of the invention are useful for
XX CC detecting a cancer in a patient, for stimulating and/or expanding T-cells
XX CC specific for a tumour protein, and for inhibiting the development of a
XX CC cancer in a patient. They are also useful for stimulating an immune
XX CC response in a patient, and for treating a cancer in a patient. The isolated
XX CC polynucleotides of the invention are useful for their ability to
XX CC selectively form duplex molecules with complementary stretches of the
XX CC entire desired gene or gene fragments, and for designing and preparing
XX CC ribozyme molecules for inhibiting expression of tumour polypeptides in
XX CC tumour cells. Polypeptides and polynucleotides of the invention are also
XX CC useful in recombinant DNA molecules to direct expression of a polypeptide
XX CC in appropriate host cells. The sequences given in records ABL48760-
XX CC ABL48956 represent polynucleotides encoding ovarian carcinoma proteins
XX SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 10
ABT03091/c
ID ABT03091 standard; cDNA; 396 BP.
XX AC ABT03091;
XX DT 05-SEP-2002 (first entry)
XX DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 15.
XX KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX KW cytostatic; gene; ss.
XX OS Homo sapiens.
XX PN WO200239885-A2.
XX PD 23-MAY-2002.
XX PF 13-NOV-2001; 2001WO-US045395.
XX PR 14-NOV-2000; 2000US-00713550.
XX PR 03-APR-2001; 2001US-00825294.
XX PR 02-OCT-2001; 2001US-00970966.
XX PA (CORI-) CORIXA CORP.

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PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX WPI; 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for detecting
XX the presence of ovarian cancer in a patient, and in pharmaceutical
XX compositions, e.g. vaccines, for treating ovarian cancer.
XX
XX Example 1; Page 117; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention
XX
XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;
XX
XX Query Match 100.0%; Score 21; DB 6; Length 396;
XX Best Local Similarity 100.0%; Pred. No. 12;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 11
ADM10684/c
ID ADM10684 standard; cDNA; 396 BP.
XX
XX ADM10684;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian carcinoma-associated cDNA 23657.1.
XX
XX ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX cytostatic; gene therapy; human; ss.
XX
XX Homo sapiens.
XX
XX US2003206918-A1.
XX
XX 06-NOV-2003.
XX
XX 05-FEB-2003; 2003US-00361811.
XX
XX 10-SEP-1999; 99US-00394374.
XX
XX 01-MAY-2000; 2000US-00561778.
XX
XX 15-AUG-2000; 2000US-00640173.
XX
XX 07-SEP-2000; 2000US-00656668.
XX
XX 14-NOV-2000; 2000US-00713550.
XX
XX 03-APR-2001; 2001US-00825294.
XX
XX 02-OCT-2001; 2001US-00970966.
XX
XX 02-AUG-2002; 2002US-00212677.
XX
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Fling SP;
XX
XX WPI; 2003-901037/82.
XX
XX New polynucleotides encoding tumor proteins, treating or inhibiting the
XX development of cancer, particularly ovarian cancer, and for stimulating
XX and/or expanding T cells specific for a tumor protein.
XX
XX Example 1; SEQ ID NO 15; 221pp; English.
XX
XX This invention describes a novel ovarian tumour protein which can be used
XX to detecting the presence of an ovarian cancer in a patient by
XX stimulating and/or expanding T cells specific for the tumour protein. The
XX products of the invention can also be used in a method to inhibit the
XX development of a cancer in a patient comprising (a) incubating CD4+

PI Ku J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX WPI; 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for detecting
XX the presence of ovarian cancer in a patient, and in pharmaceutical
XX compositions, e.g. vaccines, for treating ovarian cancer.
XX
XX Example 1; Page 117; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention
XX
XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;
XX
XX Query Match 100.0%; Score 21; DB 11; Length 396;
XX Best Local Similarity 100.0%; Pred. No. 12;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 12
ADM11014/c
ID ADJ11014 standard; cDNA; 396 BP.
XX
XX ADJ11014;
XX
XX 15-APR-2004 (first entry)
XX
XX Representative human ovarian carcinoma cDNA SeqID 15.
XX
XX human; ss; ovarian cancer; immunogenic; antibody;
XX antigen presenting cell; APC; immune system cell; T cell; tumorigenic;
XX cytostatic.
XX
XX Homo sapiens.
XX
XX US2003232056-A1.
XX
XX 18-DEC-2003.
XX
XX 14-FEB-2003; 2003US-00369186.
XX
XX 10-SEP-1999; 99US-00394374.
XX
XX 01-MAY-2000; 2000US-00561778.
XX
XX 15-AUG-2000; 2000US-00640173.
XX
XX 07-SEP-2000; 2000US-00656668.
XX
XX 14-NOV-2000; 2000US-00713550.
XX
XX 03-APR-2001; 2001US-00825294.
XX
XX 02-OCT-2001; 2001US-00970966.
XX
XX 02-AUG-2002; 2002US-00212677.
XX
XX 05-FEB-2003; 2003US-00361811.
XX
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Fling SP;
XX
XX WPI; 2004-178717/17.
XX
XX Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
XX polypeptide, useful as probes of primers for detecting presence of cancer
XX in a patient.
XX
XX Example 1; SEQ ID NO 15; 222pp; English.
XX
XX This invention relates to novel isolated polynucleotides and methods for
XX the therapy and diagnosis of cancer, particularly ovarian cancer.
XX Specifically, it refers to these polynucleotides and the encoded
XX polypeptides thereof, as well as immunogenic peptides, antibodies,
XX antigen presenting cells (APCs) and immune system cells (e.g. T cells)
XX that are targeted to those cells expressing the proteins of interest. The
XX present invention describes methods that are useful for stimulating and/
XX or expanding T cells specific for a tumorigenic protein (i.e. T cell
XX therapy). Furthermore, compositions can be used for the diagnosis
XX treatment and/ or prevention of ovarian cancer by stimulating an immune

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CC response in a patient. Accordingly, these compositions exhibit cytostatic
CC activity. This polynucleotide sequence is a representative human ovarian
CC carcinoma cDNA sequence of the invention.

XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 12; Length 396;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21

Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 13

ADM43275/c

ID ADM43275 standard; cDNA; 396 BP.

XX AC

XX ADM43275;

XX 03-JUN-2004 (first entry)

XX Human ovarian carcinoma cDNA #15.

XX ss; human; cancer; ovarian cancer; ovarian carcinoma.

XX Homo sapiens.

XX US2003129192-A1.

XX 10-JUL-2003.

XX 02-AUG-2002; 2002US-00212677.

XX 10-SEP-1999; 99US-00394374.

XX 01-MAY-2000; 2000US-00561778.

XX 15-AUG-2000; 2000US-00640173.

XX 07-SEP-2000; 2000US-00656668.

XX 14-NOV-2000; 2000US-00713550.

XX 03-APR-2001; 2001US-00825294.

XX 02-OCT-2001; 2001US-00970966.

XX (CORI-) CORIXA CORP.

XX Chenault RA, Xu J, Fanger GR, Harlocker SL, Moneill PD;

XX WPI; 2004-051070/05.

XX New isolated polynucleotide encoding an ovarian tumor protein for use in
XX diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX Example 1; SEQ ID NO 15; 220pp; English.

XX The invention relates to an isolated polynucleotide. The invention is

XX used to diagnose, prevent or treat cancer, particularly ovarian cancer.

XX The present sequence represents a human ovarian carcinoma cDNA.

XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 12; Length 396;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21

Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 14

ACH44960/c

ID ACH44960 standard; cDNA; 461 BP.

XX

AC ACH44960;

XX 13-OCT-2003 (first entry)

XX Human foetal brain cDNA #5685.

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.

XX Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

XX (LABA/) LABAT I.

XX (STAC/) STACHE-CRAIN B.

XX (DICK/) DICKSON M C.

XX (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/59.

XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.

XX Claim 1; SEQ ID NO 32172; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623

XX Sequence 461 BP; 139 A; 98 C; 144 G; 71 T; 0 U; 9 Other;

Query Match 100.0%; Score 21; DB 9; Length 461;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21

Db 130 CAGCAGCAGAGTCTTCATCAT 110

RESULT 15

ACH15312/c

ID ACH15312 standard; cDNA; 462 BP.

XX ACH15312;

XX 13-OCT-2003 (first entry)

XX

DE Human adult brain cDNA #2524.
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
OS
XX US2003073623-A1.
PN
XX 17-APR-2003.
PD
XX 30-JUL-2001; 2001US-00918995.
PF
XX 30-JUL-2001; 2001US-00918995.
PR
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STACH/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI WPI; 2003-615964/58.
DR
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 2524; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030073623
XX
SQ Sequence 462 BP; 146 A; 100 C; 142 G; 72 T; 0 U; 2 Other;

Query Match 100.0%; Score 21; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
Db 115 CAGCAGCAGAGCTTCATCAT 95

Search completed: March 22, 2005, 10:05:03
Job time : 238 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 09:42:30 ; Search time 88 Seconds
(without alignments)
390.475 Million cell updates/sec

Title: US-10-646-391A-4

Perfect score: 21

Sequence: 1 cagcagcagagtcctcatcat 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCUTS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	100.0	181	2	US-08-485-657A-19
C 2	21	100.0	181	4	US-09-366-380-19
C 3	21	100.0	181	5	PCT-US95-02303-18
C 4	21	100.0	195	2	US-08-485-657A-14
C 5	21	100.0	195	4	US-09-366-380-14
C 6	21	100.0	195	5	PCT-US95-02303-14
C 7	21	100.0	275	4	US-09-513-999C-11015
C 8	21	100.0	396	4	US-09-640-173-15
C 9	21	100.0	396	4	US-09-713-550-15
C 10	21	100.0	396	4	US-09-825-294-15
C 11	21	100.0	396	4	US-09-970-966-15
C 12	21	100.0	482	4	US-09-621-976-13267
C 13	21	100.0	491	4	US-09-513-999C-3749
C 14	21	100.0	601	4	US-09-949-016-201815
C 15	21	100.0	1648	3	US-09-659-791A-3
C 16	21	100.0	1651	3	US-09-659-791A-13
C 17	21	100.0	1825	4	US-09-949-016-5661
C 18	21	100.0	7610	3	US-09-659-791A-12
C 19	21	100.0	17348	4	US-09-949-016-17403
C 20	17.8	84.8	50	4	US-09-485-632B-15
C 21	17.8	84.8	448	4	US-09-513-999C-14310
C 22	17.8	84.8	601	4	US-09-949-016-139518
C 23	17.8	84.8	117001	4	US-09-949-016-15684
C 24	17.4	82.9	492	4	US-09-621-976-3772
C 25	17.4	82.9	633	3	US-08-950-925-1
C 26	17.4	82.9	633	4	US-09-565-286-1
C 27	17.4	82.9	651	2	US-08-961-858-1

C 28	17.4	82.9	651	2	US-08-961-858-3	Sequence 3, Appli
C 29	17.4	82.9	651	3	US-09-089-593-1	Sequence 1, Appli
C 30	17.4	82.9	651	3	US-09-089-593-3	Sequence 3, Appli
C 31	17.4	82.9	651	3	US-08-993-380-5	Sequence 5, Appli
C 32	17.4	82.9	744	4	US-09-368-819A-1	Sequence 1, Appli
C 33	17.4	82.9	785	4	US-09-949-016-2557	Sequence 2557, Ap
C 34	17.4	82.9	795	4	US-09-368-819A-3	Sequence 3, Appli
C 35	17.4	82.9	1173	3	US-08-993-380-3	Sequence 3, Appli
C 36	17.2	81.9	181	4	US-09-513-999C-26550	Sequence 26550, A
C 37	16.8	80.0	198	4	US-09-248-796A-8114	Sequence 8114, Ap
C 38	16.8	80.0	234	4	US-09-248-796A-11572	Sequence 11572, A
C 39	16.8	80.0	330	2	US-08-980-060-9	Sequence 9, Appli
C 40	16.8	80.0	330	3	US-09-307-185-9	Sequence 9, Appli
C 41	16.8	80.0	330	4	US-09-773-753-9	Sequence 9, Appli
C 42	16.8	80.0	334	3	US-09-227-357-90	Sequence 90, Appli
C 43	16.8	80.0	601	4	US-09-949-016-173228	Sequence 173228,
C 44	16.8	80.0	601	4	US-09-949-016-173229	Sequence 173229,
C 45	16.8	80.0	1806	2	US-08-980-060-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-485-657A-19/c
; Sequence 19, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-485-657A-19

Query Match 100.0%; Score 21; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCCTCATCAT 21
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Db      73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 2
US-09-366-380-19/c
Sequence 19, Application US/09366380
Patent No. 6541603
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,380
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,900
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 6541603nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-366-380-19

Query Match      100.0%; Score 21; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
Db      73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 3
PCT-US95-02303-18/c
Sequence 18, Application PC/TUS9502303
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:

US-09-366-380-19/c
Sequence 14, Application US/08485657A
Patent No. 5942389
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-485-657A-14

Query Match      100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
Db      87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 4
US-08-485-657A-14/c
Sequence 14, Application US/08485657A
Patent No. 5942389
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-485-657A-14

Query Match      100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
Db      87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 5

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US-09-366-380-14/c
; Sequence 14, Application US/09366380
; Patent No. 6541603
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Robinson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6541603nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-09-366-380-14

Query Match 100.0%; Score 21; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 6
PCT-US95-02303-14/c
; Sequence 14, Application PC/TUS9502303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02303
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
PCT-US95-02303-14

Query Match 100.0%; Score 21; DB 5; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 7
US-09-513-999C-11015/c
; Sequence 11015, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11015
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-11015

Query Match 100.0%; Score 21; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 128 CAGCAGCAGAGTCTTCATCAT 108

RESULT 8
US-09-640-173-15/c
; Sequence 15, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-15

Query Match 100.0%; Score 21; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.1;

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 9

US-09-713-550-15/c
; Sequence 15, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-15

Query Match 100.0%; Score 21; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 10

US-09-825-294-15/c
; Sequence 15, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-15

Query Match 100.0%; Score 21; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 11

US-09-970-966-15/c
; Sequence 15, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolck, John A.
; APPLICANT: Molesch, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-15

Query Match 100.0%; Score 21; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 12

US-09-621-976-13267/c
; Sequence 13267, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13267
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13267

Query Match 100.0%; Score 21; DB 4; Length 482;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 96 CAGCAGCAGAGTCTTCATCAT 76

RESULT 13

US-09-513-999C-3749/c
; Sequence 3749, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

```
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783361
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3749
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 108..455
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 108..161
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq LLFVGLLLTWESG/QV
;"
; NAME/KEY: misc_feature
; LOCATION: 459
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-3749

Query Match      100.0%; Score 21; DB 4; Length 491;
Best Local Similarity 100.0%; Pred.No. 4.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1   CAGCAGCAGAGCTCTTCATCAT 21
         |||||||
DB      128  CAGCAGCAGAGCTCTTCATCAT 108

RESULT 14
US-09-949-016-201815
; Sequence 201815, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201815
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-201815

Query Match      100.0%; Score 21; DB 4; Length 601;
Best Local Similarity 100.0%; Pred.No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1   CAGCAGCAGAGCTCTTCATCAT 21
         |||||||
DB      548  CAGCAGCAGAGCTCTTCATCAT 568

RESULT 15
US-09-659-791A-3/c
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This Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 10:02:41 ; Search time 281 Seconds
(without alignments)
444.903 Million cell updates/sec

Title: US-10-646-391A-4

Perfect score: 21

Sequence: 1 cagcagcagagtcttcattcat 21

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Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : Published Applications NA:*

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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

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18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	9	US-09-944-326-4
2	21	100.0	21	10	US-09-967-726A-4
3	21	100.0	21	16	US-10-080-794-4
4	21	100.0	21	17	US-10-646-391A-4
5	21	100.0	21	18	US-10-828-394-5
6	21	100.0	21	18	US-10-828-395-5
7	21	100.0	23	17	US-10-646-436-66
8	21	100.0	181	17	US-10-404-579-19
9	21	100.0	195	17	US-10-404-579-14
10	21	100.0	255	17	US-10-242-535A-37963
11	21	100.0	255	17	US-10-085-783A-37963

c 12	21	100.0	270	17	US-10-242-535A-33018	Sequence 33018, A
c 13	21	100.0	270	17	US-10-085-783A-33018	Sequence 33018, A
c 14	21	100.0	306	17	US-10-242-535A-28941	Sequence 28941, A
c 15	21	100.0	306	17	US-10-085-783A-28941	Sequence 28941, A
c 16	21	100.0	346	19	US-10-696-639-2963	Sequence 2963, Ap
c 17	21	100.0	386	9	US-09-825-294-15	Sequence 15, Appl
c 18	21	100.0	396	9	US-09-970-966-15	Sequence 15, Appl
c 19	21	100.0	396	15	US-10-212-677-15	Sequence 15, Appl
c 20	21	100.0	396	17	US-10-361-811-15	Sequence 15, Appl
c 21	21	100.0	396	17	US-10-369-186-15	Sequence 15, Appl
c 22	21	100.0	461	10	US-09-918-995-32172	Sequence 32172, A
c 23	21	100.0	462	10	US-09-918-995-2524	Sequence 2524, Ap
c 24	21	100.0	465	10	US-09-918-995-32177	Sequence 32177, A
c 25	21	100.0	490	10	US-09-918-995-12511	Sequence 12511, A
c 26	21	100.0	491	10	US-09-918-995-17455	Sequence 17455, A
c 27	21	100.0	492	10	US-09-918-995-31156	Sequence 31156, A
c 28	21	100.0	704	17	US-10-264-049-1985	Sequence 1985, Ap
c 29	21	100.0	1067	19	US-10-491-213-91	Sequence 91, Appl
c 30	21	100.0	1117	19	US-10-491-213-93	Sequence 93, Appl
c 31	21	100.0	1315	19	US-10-491-213-101	Sequence 101, Appl
c 32	21	100.0	1369	19	US-10-491-213-90	Sequence 90, Appl
c 33	21	100.0	1373	19	US-10-491-213-102	Sequence 102, Appl
c 34	21	100.0	1451	16	US-10-133-013-214	Sequence 214, Appl
c 35	21	100.0	1568	17	US-10-221-178-29	Sequence 29, Appl
c 36	21	100.0	1568	17	US-10-221-178-29	Sequence 29, Appl
c 37	21	100.0	1610	19	US-10-491-213-89	Sequence 89, Appl
c 38	21	100.0	1614	16	US-10-119-428-31	Sequence 31, Appl
c 39	21	100.0	1648	17	US-10-380-124-3	Sequence 3, Appl
c 40	21	100.0	1651	17	US-10-380-124-13	Sequence 13, Appl
c 41	21	100.0	1651	18	US-10-717-597-63	Sequence 63, Appl
c 42	21	100.0	1651	19	US-10-278-698-139	Sequence 139, App
c 43	21	100.0	1651	19	US-10-278-698-655	Sequence 655, App
c 44	21	100.0	1676	17	US-10-646-391A-1	Sequence 1, Appl
c 45	21	100.0	1676	18	US-10-283-975A-259	Sequence 259, App

ALIGNMENTS

RESULT 1

US-09-944-326-4 ; Sequence 4, Application US/09944326

Patent No. US20020128220A1 ; GENERAL INFORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Rennie, Paul S.

APPLICANT: Miyake, Hideaki

APPLICANT: Nelson, Colleen

TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY

FILE REFERENCE: UBC.P-020-2

CURRENT APPLICATION NUMBER: US/09/944,326

CURRENT FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: 60/121,726

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 09/913,325

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 21

TYPE: DNA

ORGANISM: HUMAN

FEATURE:

OTHER INFORMATION: antisense TRPM-2 ODN

US-09-944-326-4

Query Match 100.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21

Db 1 CAGCAGCAGAGTCTTCATCAT 21

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RESULT 2
US-09-967-726A-4
; Sequence 4, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-4

Query Match      100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 3
US-10-080-794-4
; Sequence 4, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-4

Query Match      100.0%; Score 21; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 1 CAGCAGCAGAGTCTTCATCAT 21
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RESULT 4
US-10-646-391A-4
; Sequence 4, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-4

Query Match      100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 5
US-10-828-394-5
; Sequence 5, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-5

Query Match      100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
   |||||
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 6
US-10-828-395-5
; Sequence 5, Application US/10828395
; Publication No. US20040224914A1
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GENERAL INFORMATION:
APPLICANT: Jackson, John
APPLICANT: Burt, Helen
APPLICANT: Springate, Christopher
APPLICANT: Gleave, Martin
TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
FILE REFERENCE: UBC.P-032
CURRENT APPLICATION NUMBER: US/10/828,395
CURRENT FILING DATE: 2004-04-19
PRIOR APPLICATION NUMBER: US 60/464,159
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: US 60/464,160
PRIOR FILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 21
TYPE: DNA
ORGANISM: human
US-10-828-395-5

Query Match 100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 7
US-10-646-436-66/c
Sequence 66, Application US/10646436
Publication No. US20040096882A1
GENERAL INFORMATION:
APPLICANT: Jansen, Burkhard
APPLICANT: Gleave, Martin
APPLICANT: Signaevsky, Maxim
APPLICANT: Betaldi, Eliana
APPLICANT: Trougakos, Ioannis
APPLICANT: Gonos, Efsthachios
TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
FILE REFERENCE: UBC.P-030
CURRENT APPLICATION NUMBER: US/10/646,436
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: US 60/405,193
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/408,152
PRIOR FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US 60/473,387
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66
LENGTH: 23
TYPE: DNA
ORGANISM: human
US-10-646-436-66

Query Match 100.0%; Score 21; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 23 CAGCAGCAGAGTCTTCATCAT 3

RESULT 8
US-10-404-579-19/c
Sequence 19, Application US/10404579
Publication No. US20040002099A1
GENERAL INFORMATION:

APPLICANT: Kirschling, Deborah J
Gudkov, Andrei
Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/404,579
FILING DATE: 01-Apr-2003
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. US20040002099A1nhan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-404-579-19

Query Match 100.0%; Score 21; DB 17; Length 181;
Best Local Similarity 100.0%; Pred. No. 4; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 9
US-10-404-579-14/c
Sequence 14, Application US/10404579
Publication No. US20040002099A1
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
Gudkov, Andrei
Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/404,579
FILING DATE: 01-Apr-2003
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: NO. US2004002099Alnan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-404-579-14

Query Match 100.0%; Score 21; DB 17; Length 195;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 10
US-10-242-535A-37963/c
; Sequence 37963, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37963
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-37963

Query Match 100.0%; Score 21; DB 17; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 97 CAGCAGCAGAGTCTTCATCAT 77

RESULT 11

US-10-085-783A-37963/c
; Sequence 37963, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37963
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-37963

Query Match 100.0%; Score 21; DB 17; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 97 CAGCAGCAGAGTCTTCATCAT 77

RESULT 12
US-10-242-535A-33018/c
; Sequence 33018, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33018
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-33018

Query Match 100.0%; Score 21; DB 17; Length 270;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
DB 62 CAGCAGCAGAGTCTTCATCAT 42

RESULT 13
US-10-085-783A-33018/c
; Sequence 33018, Application US/10085783A
; Publication No. US20040037841A1

; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 33018
 ; LENGTH: 270
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-085-783A-33018

Query Match 100.0%; Score 21; DB 17; Length 270;
 * Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
 Db 62 CAGCAGCAGAGTCTTCATCAT 42

RESULT 14
 US-10-242-535A-28941/c
 ; Sequence 28941, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT APPLICATION NUMBER: US/10/242,535A
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 28941
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-242-535A-28941

Query Match 100.0%; Score 21; DB 17; Length 306;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
 Db 98 CAGCAGCAGAGTCTTCATCAT 78

RESULT 15
 US-10-085-783A-28941/c
 ; Sequence 28941, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 28941
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-085-783A-28941

Query Match 100.0%; Score 21; DB 17; Length 306;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
 Db 98 CAGCAGCAGAGTCTTCATCAT 78

Search completed: March 22, 2005, 11:04:23
 Job time : 281 secs

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This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 09:35:40 ; Search time 1737 Seconds
(without alignments)
460.190 Million cell updates/sec

Title: US-10-646-391A-4

Perfect score: 21

Sequence: 1 cagcagcagagtcttcacat 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	85	2	AW276802 xp6a01.x
2	21	100.0	100	2	BF920141 MR1-NT017
3	21	100.0	102	4	BF958934 PM1-NN120
4	21	100.0	119	2	AW901233 CM4-NN101
5	21	100.0	124	4	EM821731 K-EST0090
6	21	100.0	136	6	CD612966 56043322J
7	21	100.0	137	6	CD612965 56043322H
8	21	100.0	138	5	BQ339862 PM1-NN120
9	21	100.0	142	7	D45267 HUMHG1194.H
10	21	100.0	147	5	BQ339466 PM1-NN120
11	21	100.0	148	2	BF846357 PM1-EN006
12	21	100.0	149	7	R47195 CBS-389 Sub
13	21	100.0	169	2	BE766895 RC2-NT011
14	21	100.0	177	1	AL048592 DKFP586H
15	21	100.0	183	4	BT032792 MR4-NN018
16	21	100.0	184	4	BF958930 PM1-NN120
17	21	100.0	185	4	BT036860 MR4-NT014
18	21	100.0	196	1	AI745406 wc37D01.x
19	21	100.0	197	4	BT036862 MR4-NT014
20	21	100.0	201	4	BF957666 PM1-NN120
21	21	100.0	203	4	BF957653 PM1-NN120
22	21	100.0	207	4	BF957858 PM1-NN120
23	21	100.0	224	2	AW161224 au70a10.y
24	21	100.0	226	2	BF935119 MR4-NT014

25	21	100.0	236	4	BF948789	MR3-NN021
26	21	100.0	238	2	BF923639	MR4-NT014
27	21	100.0	239	4	BF958974	HOA21-1-C
28	21	100.0	241	7	CR767137	DKFP469B
29	21	100.0	243	1	AA336628	EST41242
30	21	100.0	244	2	BE766870	RC2-NT011
31	21	100.0	248	2	BF923643	MR4-NT014
32	21	100.0	249	4	BF945175	PM1-NN120
33	21	100.0	250	5	BQ345410	MR4-NT014
34	21	100.0	252	2	BF923633	MR4-NT014
35	21	100.0	252	4	BF963107	PM1-NN120
36	21	100.0	253	2	BF887875	OV2-TN017
37	21	100.0	253	4	BT041998	MR4-NT014
38	21	100.0	256	4	BT041248	MR4-NT014
39	21	100.0	257	6	CD612964	56037472J
40	21	100.0	258	4	BF961150	PM1-NN120
41	21	100.0	258	7	CR763018	DKFP469G
42	21	100.0	262	4	BF947155	MR3-NN021
43	21	100.0	262	5	BQ339859	PM1-NN120
44	21	100.0	263	2	BE899032	601682590
45	21	100.0	265	4	BF961152	PM1-NN120

ALIGNMENTS

RESULT 1
AW276802/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW276802

xp6a01.x1 NCI CGAP Ov39 Homo sapiens cDNA clone IMAGE:2745288 3'

similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.

AW276802

AW276802.1 GI:6663832

EST.

Homo sapiens (human)

Homo sapiens

1 (bases 1 to 85)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: Andrew Berchuck M.D., John Gillespie M.D.,

Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco.

Location/Qualifiers

1..85

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2745288"

/sex="female"

/tissue_type="papillary serous ovarian metastasis"

/lab_host="DH10B"

/clone_lib="NCI CGAP Ov39"

/notes="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT

priming. Non-directionally cloned into the UDG sites of

pAMP10. Size-selected on agarose gel, average insert

size 500 bp. Primary library; non-amplified cDNA

Library Preparation: David B. Krizman, Ph.D. (NCI).

Reference: Krizman et al. (1996) Cancer Research

56:5380-5383."

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
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 DB 82 CAGCAGCAGAGTCTTCATCAT 62

RESULT 2

LOCUS BF920141 100 bp mRNA linear EST 19-JAN-2001
 DEFINITION MR1-NT0179-071100-003-f02 NT0179 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF920141
 VERSION BF920141.1 GI:12316029
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 20202663
 COMMENT 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

FEATURES

source
 1..100
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0179"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 |||
 DB 56 CAGCAGCAGAGTCTTCATCAT 76

RESULT 3

LOCUS BF958934/c 102 bp mRNA linear EST 22-JAN-2001
 DEFINITION PM1-NN1200-011200-009-b07 NN1200 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF958934
 VERSION BF958934.1 GI:12376209
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 20202663
 COMMENT 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

FEATURES

source
 1..102
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NN1200"
 /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 4; Length 102;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 |||
 DB 91 CAGCAGCAGAGTCTTCATCAT 71

RESULT 4

LOCUS AW901233/c 119 bp mRNA linear EST 24-MAY-2000
 DEFINITION CM4-NN1011-100300-110-g04 NN1011 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW901233
 VERSION AW901233.1 GI:8065542
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119)

REFERENCE
AUTHORS

Das Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL
MEDLINE
PUBMED
COMMENT

20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-cm4-NN1011-100
300-110-g04t3=2000-03-10&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 11

High quality sequence stop: 118.

FEATURES
source

1..119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1011"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 103 CAGCAGCAGAGTCTTCATCAT 83

RESULT 5

BM821731/c

LOCUS

DEFINITION K-EST0090952 S20T665307 Homo sapiens cDNA clone S20T665307-15-H01
5', mRNA sequence.

ACCESSION

BM821731

VERSION

BM821731.1 GI:19178144

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 124)

REFERENCE
AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 15 row: H column: 01
High quality sequence stop: 124.

FEATURES

Location/Qualifiers
1..124
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-15-H01"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 21; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 102 CAGCAGCAGAGTCTTCATCAT 82

RESULT 6

CD612966

LOCUS

DEFINITION S6043322U1 FLP Homo sapiens cDNA, mRNA sequence.
136 bp mRNA linear EST 12-JAN-2004

ACCESSION

CD612966

VERSION

CD612966.1 GI:40261230

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 136)

AUTHORS

Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL

Genomics 84 (1), 205-210 (2004)

COMMENT

Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com

FEATURES

Location/Qualifiers

1..136

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 |||||
 Db 69 CAGCAGCAGAGTCTTCATCAT 89

RESULT 7
 CD612965/c
 LOCUS 56043322H1 FLP Homo sapiens cDNA, mRNA sequence. EST 12-JAN-2004

DEFINITION CD612965
 ACCESSION CD612965
 VERSION CD612965.1 GI:40261229
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 137)

AUTHORS Fu, G.-K., Wang, J.-T., Yang, J., Au-Young, J. and Stuve, L. L.

TITLE Circular rapid amplification of cDNA ends for high-throughput

JOURNAL extension cloning of partial genes

COMMENT Genomics 84 (1), 205-210 (2004)

CONTACT: Fu GK

INCYTE Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

TEL: 6508454102

EMAIL: gfu@incyte.com

LOCATION/Qualifiers

1..137

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/notes="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 137;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 |||||
 Db 68 CAGCAGCAGAGTCTTCATCAT 48

RESULT 8
 BQ339862/c
 LOCUS BQ339862 138 bp mRNA linear EST 20-MAY-2002

DEFINITION PMI-NN1200-011200-010-f07 NN1200 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ339862

VERSION BQ339862.1 GI:20999978

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 138)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,

Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, P. F.,

Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,

Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,

O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and

Simpson, A. J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=PM1&c2=PM1-NN1200-
 011200-010-f07&c3=2000-12-01&k4=1)

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence stop: 35.

FEATURES

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Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 5; Length 138;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

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Db 127 CAGCAGCAGAGTCTTCATCAT 107

RESULT 9

D45267/c

LOCUS HUMHG1194 Human cerebral cortex Homo sapiens cDNA, mRNA sequence.

DEFINITION D45267

ACCESSION D45267.1 GI:1136645

VERSION EST.

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 142)

AUTHORS Takahashi, N., Hashida, H., Zhao, N., Misumi, Y. and Sakaki, Y.

TITLE High-density cDNA filter analysis of the expression profiles of the

genes preferentially expressed in human brain

JOURNAL Gene 164, 219-227 (1995)

MEDLINE 96069586

PUBMED 7590334

COMMENT Contact: Nobuaki Takahashi

Institute of Medical Science

University of Tokyo

Shirokaned 4-6-1, Minato-ku, Tokyo, Japan 108

Tel: 03-5449-5625

Fax: 03-5449-5445

LOCATION/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="Human cerebral cortex"

/note="Adult male cerebral cortex tissue."

FEATURES

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1..142

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Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 79 CAGCAGCAGAGTCTTCATCAT 59

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LOCUS
DEFINITION PM1-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ339466
VERSION BQ339466.1 GI:20999152
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-
051100-004-h12&t3=2000-11-05&t4=1)
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High quality sequence stop: 34.
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        /clone_lib="NN1200"
    /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
    Site_2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196,716 - Ludwig Institute for Cancer Research)
    profiles into the pUC 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 122 CAGCAGCAGAGTCTTCATCAT 142

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LOCUS
DEFINITION PM1-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ339466
VERSION BQ339466.1 GI:20999152
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-
051100-004-h12&t3=2000-11-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 34.
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    Site_2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196,716 - Ludwig Institute for Cancer Research)
    profiles into the pUC 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."

ORIGIN
Query Match 100.0%; Score 21; DB 5; Length 147;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 122 CAGCAGCAGAGTCTTCATCAT 142

RESULT 12
R47195/c
LOCUS
DEFINITION CBS-389 Subtractive cDNA library ocular ciliary body Homo sapiens
cDNA clone CBS-389 5' end similar to TRPM-2 (clusterin) (accession
number M64722), mRNA sequence.
ACCESSION R47195
VERSION R47195.1 GI:807537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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LOCUS
DEFINITION PM1-EN0065-231000-002-b01 EN0065 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF846357
VERSION BF846357.1 GI:12233611
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-EN0065-
231000-002-b01&t3=2000-10-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 110.
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    /note="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
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    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196,716 - Ludwig Institute for Cancer Research)
    profiles into the pUC 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."

ORIGIN
Query Match 100.0%; Score 21; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 34 CAGCAGCAGAGTCTTCATCAT 54

RESULT 12
R47195/c
LOCUS
DEFINITION CBS-389 Subtractive cDNA library ocular ciliary body Homo sapiens
cDNA clone CBS-389 5' end similar to TRPM-2 (clusterin) (accession
number M64722), mRNA sequence.
ACCESSION R47195
VERSION R47195.1 GI:807537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS      Escrignano,J., Ortego,J. and Coca-Prados,M.
TITLE        Isolation and characterization of cell-specific cDNA clones from a
              subtractive library of the ocular ciliary body of a single normal
              human donor: Transcription and synthesis of plasma proteins
JOURNAL      J. Biochem. 118 (5), 921-931 (1995)
MEDLINE      96318503
PUBMED       8749308
COMMENT      Contact: Coca-Prados, M.
              Department of Ophthalmology and Visual Science
              Yale University Medical School
              330 Cedar Street, New Haven, CT 06520-8061
              Tel: 2037852742
              Fax: 2037856123
              Email: miguel.coca-prados@quickmail.yale.edu
              Seq primer: T3.
              Location/Qualifiers
FEATURES
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              (ssDNA) (as pBluescript SK-) from the ocular ciliary body
              cDNA library (target) of a 34-year-old female donor in
              lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular
              cell line cDNA library (driver) in the same vector."
ORIGIN
Query Match 100.0%; Score 21; DB 7; Length 149;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE766895
VERSION     BE766895.1 GI:10196819
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 169)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC2-NT0110-050
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High quality sequence stop: 169.
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              Site 2: SmaI; A mini-library was made by cloning products
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              No. 196,716 - Ludwig Institute for Cancer Research)
              profiles into the puc 18 vector. Reverse transcription of
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              low stringency conditions."
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Db 59 CAGCAGCAGAGTCTTCATCAT 39

RESULT 14
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LOCUS       AL048592 177 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFP586H092_r1 586 (synonym: hutel) Homo sapiens cDNA clone
ACCESSION  AL048592
VERSION     AL048592.1 GI:4729143
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 177)
AUTHORS     Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
              EST (Poustka, et al.)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: MIPS
              MIPS
              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
              This is the 5' sequence of the clone insert
              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
              Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
              sequenced by DKFZ (German Cancer Research Center,
              Heidelberg/Germany) within the cDNA sequencing consortium of the
              German Genome Project.
              No sl sequence available.
              This clone (DKFP586H092) is available at the RZPD in Berlin.
              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
              Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
              Location/Qualifiers
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 Db 77 CAGCAGCAGAGTCTTCATCAT 57

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 DEFINITION
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 VERSION BI032792.1 GI:14439418
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 183)
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&st2=MR4-NN0188-220101-204-e01&t3=2001-01-22&t4=1>)
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 High quality sequence stop: 183.

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 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
 Query Match 100.0%; Score 21; DB 4; Length 183;
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: March 22, 2005, 10:58:03
 Job time : 1740 secs

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